

# EXHIBIT 16

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

☒ Use Mega BLAST Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DTGNSFYESTULTHALSSQFMLSISEASUNQLKSDUUFSGNLNVPHTGWQGLWSGWAKIQ
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLAKLVGLYSYGDHNCCHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFPMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

VAGLEKDPVA

PT 7CT2

Murder  
Enf. Immunity  
61:4406, 1993

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Align**Sequence 1 |cl|seq\_1 Length 955 *PHPO clone ATCC PTA 2462*Sequence 2 |cl|seq\_2 Length 10 *PTTCTZ*

No significant similarity was found

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Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DYGNSTYESTDLTRALSSQFLSLSEASUNQLRSDUUFSGNLNVPHTGWQGLWSWGMAKTV
DPEPASSATITDPKANKRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTGGENLTSQGT
FRSQTMGGAVFFDLPMKPPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSPSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

PTSDVAGLEKDFVA

PT 7 C + 4

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq\_1 Length 955 **PMPE ATCC PTA 2462**

Sequence 2 lcl|seq\_2 Length 15 **PT7C4**

No significant similarity was found

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  Matrix

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

☒ Use **Mega BLAST** Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DYGNSTYESTDTHALSSQFMLSISEASDQLKRSDDMDFSGLNVFHYGWQLWSWGWAQV  
DPEPASSATITDPKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS  
AELTPSDHPPFWGITGGGLGMVYQEPRENHPPGFMHRSSGYFAGMIAGQTHTFSLKFSQTYT  
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTOGENLTSQGT  
FRSQTMGGAVFFDLPMKFFGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSFSTKTPLINV  
LVPIGVKGSFMNATQRPQAWTVELAYQFVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS  
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

PTTSDVAGLEKDPKD

PT 7e+5

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

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Matrix: **BLOSUM62** gap open: **11** gap extension: **1**

x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq\_1 Length 955 **PMPE ATCC PTA 2462**

Sequence 2 lcl|seq\_2 Length 15 **PT7CTS**

No significant similarity was found

## BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

**Reference:** Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", *FEMS Microbiol Lett.* 174:247-250

Program  Matrix

Parameters used in **BLASTN** program only:

Reward for a match:  Penalty for a mismatch:

☒ Use **Mega BLAST** Strand option

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DTGNSFTESTLTHALSSQPLSLSEASLNQLKSDUMDFSGNLNVPHTGWQLWSDGWAKTV
DPEPASSATITDPKKNRFRHTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGVFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQCGEMLSLQEGFLAKLVGLYSYGDHNCCHFYTGGENLTSQGT
FRSQTMGGAFFDLPMKPPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

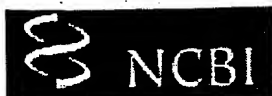
or sequence in FASTA format from:  to:

```
NPASTTSDVAGLEKDPVA
```

PTCT7

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## Blast 2 Sequences results

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq\_1 Length 955

Sequence 2 lcl|seq\_2 Length 18

No significant similarity was found

PMPE clone PTA 2462  
~~PTA 2462~~ PTA 2462

## BLAST 2 SEQUENCES

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Program  Matrix

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Reward for a match:  Penalty for a mismatch:

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Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter ☒

Sequence 1 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
DYGNSTFESTDLTRALSSQFMLSISEASUNQLRSDDMFSGNLNVPHYGWQLWSGWAKTQ
DPEPASSATITDPKKNRPHRTLLLTWLPAGYVFPSPKHSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMLAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSQCQEMFLSLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTVEGAYPRSPSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI  or download from file

or sequence in FASTA format from:  to:

```
NPASTTSDVAGLEKDEPKD
```

P-T7C+8

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## Blast 2 Sequences results

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Matrix: **BLOSUM62** gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.0** wordsize: **3** Filter: ☒ **Align**Sequence 1 lcl|seq\_1 Length 955 **PMPE ATCC PTA 2462**Sequence 2 lcl|seq\_2 Length 18 **PTTCT**

No significant similarity was found